OIPE

RAW SEQUENCE LISTING   DATE: 08/08/2001
PATENT APPLICATION: US/09/919,585   TIME: 11:44:01

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\08082001\I919585.raw

ENTERED

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 4 <110> APPLICANT: Sun, Tian-Qiang
 5         Feng, Jia-Jia
 6         Reinhard, Christoph
 7         Fantl, Wendy J.
 8         Williams, Lewis T.
11 <120> TITLE OF INVENTION: ISOLATION OF DROSOPHILA AND HUMAN POLYNUCLEOTIDES ENCODING
PAR-1 KINASE,
12         POLYPEPTIDES ENCODED BY THE POLYNUCLEOTIDES AND METHODS UTILIZING THE
13         POLYNUCLEOTIDES AND POLYPEPTIDES
16 <130> FILE REFERENCE: PP-016093.002/200130.525
18 <140> CURRENT APPLICATION NUMBER: US/09/919,585  OK
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23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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33 tcaggagctc ggtgtagaaa ctctatagcc tcctgtgcag atgaacaacc tcacatcgga     180
34 aactacagac tgttgaaaac aatcggcaag gggaattttg caaaagtaaa attggcaaga     240
35 catatcctta caggcagaga ggttgcaata aaaataattg acaaaactca gttgaatcca     300
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38 gcaagtggag gtgaagtatt tgactatttg gttgcacatg caggatgaa ggaaaaagaa      480
39 gcaagatcta aatttagaca gattgtgtct gcagttcaat actgccatca gaaacggatc     540
40 gtacatcgag acctcaaggc tgaaaatcta ttgttagatg ccgatatgaa cattaaaata     600
41 gcagatttcg gtttttagcaa tgaatttact gttggcggta aactcgacac gttttgtggc     660
42 agtcctccat acgcagcacc tgagctcttc cagggcaaga aatatgacgg gccagaagtg     720
43 gatgtgtgga gtctgggggt cattttatac acactagtca gtggctcact tcccttttgat    780
44 gggcaaaacc taaaggaact gagagagaga gtattaagag ggaaatacag aattcccttc     840
45 tacatgtcta cagactgtga aaaccttctc aaacgtttcc tggtgctaaa tccaattaaa     900
46 cgcggcactc tagagcaaat catgaaggac aggtggatca atgcagggca tgaagaagat     960
47 gaactcaaac catttgttga accagagcta gacatctcag accaaaaaag aatagatatt    1020
48 atggtgggaa tgggatattc acaagaagaa attcaagaat ctcttagtaa gatgaaatac    1080
49 gatgaaatca cagctacata tttgttattg gggagaaaat cttcagagct ggatgctagt    1140
50 gattccagtt ctagcagcaa tctttcactt gctaaggtta ggccgagcag tgatctcaac    1200
51 aacagtactg gccagtctcc tcaccacaaa gtgcagagaa gtgtttcttc aagccaaaag    1260
52 caaagacgct acagtgacca tgctggacca gctattcctt ctgttgtggc gtatccgaaa    1320
53 aggagtcaga ccagcactgc agatagtgac ctcaaagaag atggaatttc ctcccggaaa    1380
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56 agtaacacag catctggtgg aatgacacga cgaaatactt atgtttgcag tgagagaact    1560
57 acagctgata gacactcagt gattcagaat ggcaaagaaa cagcactat tcctgatcag      1620
58 agaactccag ttgcttcaac acacagtatc agtagtgcag ccaccccaga tcgaatccgc    1680
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62 aggcttccaa ctgaatatga gaggaacggg agatatgagg gctcaagtcg caatgtatct    1920
63 gctgagcaaa aagatgaaaa caaagaagca aagcctcgat ccctacgctt cacctggagc    1980
64 atgaaaacca ctagttcaat ggatcccggg gacatgatgc gggaaatccg caaagtgttg    2040
65 gacgccaata actgcgacta tgagcagagg gagcgcttct tgctcttctg cgtccacgga    2100
66 gatgggcacg cggagaacct cgtgcagtgg gaaatggaag tgtgcaagct gccaagactg    2160
67 tctctgaacg gggtccggtt taagcggata tcggggacat ccatagcctt caaaaatatt    2220
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78 agtcctcgag ccacatcttt gagatatcgg aggacacgtc tacttgttgg agtgtagcct     180
79 ttgatgtctg acaacttttg ttagccgttc cccttaaaac gtttttcattt taaccgttct     240
80 gtataggaat gtccgtctct ccaacgttat ttttattaac tgttttgagt caacttaggt     300
81 tgttcagatg ttttcgagaa gtctcttcat tcttattact tctaaaattt agtagggtta     360
82 tatcacttca ataagcttca gtaactttgg cttttttgtg agatggatta gtaccttata     420
83 cgttcacctc cacttcataa actgataaac caacgtgtac cgtcctactt cctttttctt     480
84 cgttctagat ttaaatctgt ctaacacaga cgtcaagtta tgacggtagt ctttgcctag     540
85 catgtagctc tggagttccg acttttagat aacaatctac ggctatactt gtaattttat     600
86 cgtctaaagc caaaatcgtt acttaaatga caaccgccat ttgagctgtg caaaacaccg     660
87 tcaggaggta tgcgtcgtgg actcgagaag gtcccgttct ttatactgcc cggtcttcac     720
88 ctacacacct cagaccccca gtaaaatatg tgtgatcagt caccgagtga agggaaacta     780
89 cccgttttgg atttccttga ctctctctct cataattctc cctttatgtc ttaagggaag     840
90 atgtacagat gtctgacact tttggaagag tttgcaaagg accacgattt aggttaattt     900
91 gcgccgtgag atctcgttta gtacttcctg tccacctagt tacgtcccgt acttcttcta     960
92 cttgagtttg gtaaacaact tggtctcgat ctgtagagtc tggttttttc ttatctataa    1020
93 taccaccctt accctataag tgttcttctt taagttctta gagaatcatt ctactttatg    1080
94 ctactttagt gtcgatgtat aaacaataac ccctctttta gaagtctcga cctacgatca    1140
95 ctaaggtcaa gatcgtcgtt agaaagtgaa cgattccaat ccggctcgtc actagagttg    1200
96 ttgtcatgac cggtcagagg agtggtgttt cacgtctctt cacaaagaag ttcggttttc    1260
97 gtttctgcga tgtcactggt acgacctggt cgataaggaa gacaacaccg cataggcttt    1320
98 tcctcagtct ggtcgtgacg tctatcactg gagtttcttc taccttaaag gagggccttt    1380
99 agttcaccgt cacgacaacc tcctttccct taacgaggtc ggtcagggta cgaacccttа    1440
100 cgttcattag gattattccg cctataagga cttgcgttct tttcgaggtg acagggatca    1500
101 tcattgtgtc gtagaccacc ttactgtgct gctttatgaa tacaaacgtc actctcttga    1560
102 tgtcgactat ctgtgagtca ctaagtctta ccgtttcttt tgtcgtgata aggactagtc    1620
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106 gtctgagctt cggctccgag gtgattagag aaatcattta attgaagttt tgagtgttcc    1860
107 tccgaaggtt gacttatact ctccttgccc tctatactcc cgagttcagc gttacataga    1920
108 cgactcgttt ttctactttt gtttcttcgt ttcggagcta gggatgcgaa gtggacctcg    1980
109 tacttttggt gatcaagtta cctagggccc ctgtactacg ccctttaggc gtttcacaac    2040
110 ctgcggttat tgacgctgat actcgtctcc ctcgcgaaga acgagaagac gcaggtgcct    2100
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117 <212> TYPE: PRT
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123 Asn His Thr Ser His Gly Asp Gly Arg Gln Glu Val Thr Ser Arg Thr
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125 Ser Arg Ser Gly Ala Arg Cys Arg Asn Ser Ile Ala Ser Cys Ala Asp
126         35                  40                  45
127 Glu Gln Pro His Ile Gly Asn Tyr Arg Leu Leu Lys Thr Ile Gly Lys
128     50                  55                  60
129 Gly Asn Phe Ala Lys Val Lys Leu Ala Arg His Ile Leu Thr Gly Arg
130 65                  70                  75                  80
131 Glu Val Ala Ile Lys Ile Ile Asp Lys Thr Gln Leu Asn Pro Thr Ser
132                 85                  90                  95
133 Leu Gln Lys Leu Phe Arg Glu Val Arg Ile Met Lys Ile Leu Asn His
134             100                 105                 110
135 Pro Asn Ile Val Lys Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu
136             115                 120                 125
137 Tyr Leu Ile Met Glu Tyr Ala Ser Gly Gly Glu Val Phe Asp Tyr Leu
138     130                 135                 140
139 Val Ala His Gly Arg Met Lys Glu Lys Glu Ala Arg Ser Lys Phe Arg
140 145                 150                 155                 160
141 Gln Ile Val Ser Ala Val Gln Tyr Cys His Gln Lys Arg Ile Val His
142                 165                 170                 175
143 Arg Asp Leu Lys Ala Glu Asn Leu Leu Leu Asp Ala Asp Met Asn Ile
144             180                 185                 190
145 Lys Ile Ala Asp Phe Gly Phe Ser Asn Glu Phe Thr Val Gly Gly Lys
146             195                 200                 205
147 Leu Asp Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe
148     210                 215                 220
149 Gln Gly Lys Lys Tyr Asp Gly Pro Glu Val Asp Val Trp Ser Leu Gly
150 225                 230                 235                 240
151 Val Ile Leu Tyr Thr Leu Val Ser Gly Ser Leu Pro Phe Asp Gly Gln
152                 245                 250                 255
153 Asn Leu Lys Glu Leu Arg Glu Arg Val Leu Arg Gly Lys Tyr Arg Ile
154             260                 265                 270
155 Pro Phe Tyr Met Ser Thr Asp Cys Glu Asn Leu Leu Lys Arg Phe Leu
156         275                 280                 285
157 Val Leu Asn Pro Ile Lys Arg Gly Thr Leu Glu Gln Ile Met Lys Asp
158     290                 295                 300
159 Arg Trp Ile Asn Ala Gly His Glu Glu Asp Glu Leu Lys Pro Phe Val
160 305                 310                 315                 320
161 Glu Pro Glu Leu Asp Ile Ser Asp Gln Lys Arg Ile Asp Ile Met Val
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163 Gly Met Gly Tyr Ser Gln Glu Glu Ile Gln Glu Ser Leu Ser Lys Met
164                 340                 345                 350
165 Lys Tyr Asp Glu Ile Thr Ala Thr Tyr Leu Leu Leu Gly Arg Lys Ser
166                 355                 360                 365
167 Ser Glu Leu Asp Ala Ser Asp Ser Ser Ser Ser Ser Asn Leu Ser Leu
168                 370                 375                 380
169 Ala Lys Val Arg Pro Ser Ser Asp Leu Asn Asn Ser Thr Gly Gln Ser
170 385                 390                 395                 400
171 Pro His His Lys Val Gln Arg Ser Val Ser Ser Ser Gln Lys Gln Arg
172                 405                 410                 415
173 Arg Tyr Ser Asp His Ala Gly Pro Ala Ile Pro Ser Val Val Ala Tyr
174                 420                 425                 430
175 Pro Lys Arg Ser Gln Thr Ser Thr Ala Asp Ser Asp Leu Lys Glu Asp
176                 435                 440                 445
177 Gly Ile Ser Ser Arg Lys Ser Ser Gly Ser Ala Val Gly Gly Lys Gly
178         450                 455                 460
179 Ile Ala Pro Ala Ser Pro Met Leu Gly Asn Ala Ser Asn Pro Asn Lys
180 465                 470                 475                 480
181 Ala Asp Ile Pro Glu Arg Lys Lys Ser Ser Thr Val Pro Ser Ser Asn
182                 485                 490                 495
183 Thr Ala Ser Gly Gly Met Thr Arg Arg Asn Thr Tyr Val Cys Ser Glu
184                 500                 505                 510
185 Arg Thr Thr Ala Asp Arg His Ser Val Ile Gln Asn Gly Lys Glu Asn
186         515                 520                 525
187 Ser Thr Ile Pro Asp Gln Arg Thr Pro Val Ala Ser Thr His Ser Ile
188         530                 535                 540
189 Ser Ser Ala Ala Thr Pro Asp Arg Ile Arg Phe Pro Arg Gly Thr Ala
190 545                 550                 555                 560
191 Ser Arg Ser Thr Phe His Gly Gln Pro Arg Glu Arg Arg Thr Ala Thr
192                 565                 570                 575
193 Tyr Asn Gly Pro Pro Ala Ser Pro Ser Leu Ser His Glu Ala Thr Pro
194             580                 585                 590
195 Leu Ser Gln Thr Arg Ser Arg Gly Ser Thr Asn Leu Phe Ser Lys Leu
196         595                 600                 605
197 Thr Ser Lys Leu Thr Arg Arg Leu Pro Thr Glu Tyr Glu Arg Asn Gly
198     610                 615                 620
199 Arg Tyr Glu Gly Ser Ser Arg Asn Val Ser Ala Glu Gln Lys Asp Glu
200 625                 630                 635                 640
201 Asn Lys Glu Ala Lys Pro Arg Ser Leu Arg Phe Thr Trp Ser Met Lys
202                 645                 650                 655
203 Thr Thr Ser Ser Met Asp Pro Gly Asp Met Met Arg Glu Ile Arg Lys
204                 660                 665                 670
205 Val Leu Asp Ala Asn Asn Cys Asp Tyr Glu Gln Arg Glu Arg Phe Leu
206         675                 680                 685
207 Leu Phe Cys Val His Gly Asp Gly His Ala Glu Asn Leu Val Gln Trp
208         690                 695                 700
209 Glu Met Glu Val Cys Lys Leu Pro Arg Leu Ser Leu Asn Gly Val Arg
210 705                 710                 715                 720
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217 <211> LENGTH: 2112
218 <212> TYPE: DNA
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227 gtcatggagt acgctagtgg cggagaggta tttgattacc tagtggctca tggcaggatg     360
228 aaagaaaaag aggctcgagc caaattccgc cagatagtgt ctgctgtgca gtactgtcac     420
229 cagaagttta ttgtccatag agacttaaag gcagaaaacc tgctcttgga tgctgatatg     480
230 aacatcaaga ttgcagactt tggcttcagc aatgaattca cctttgggaa caagctggac     540
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259 <210> SEQ ID NO: 5
260 <211> LENGTH: 2112
261 <212> TYPE: DNA
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L:18 M:270 C: Current Application Number differs, Wrong Format